

November 24, 2009

To: The Data Availability Group, Secretariat of the International Whaling Commission
From: C. S. Baker, Oregon State University
Concerning: Genetic analyses of North Pacific minke whales from Korean markets for Pre-Implementation Assessment

Others and I confirm our intent to present genetic analyses of North Pacific minke whale products purchased during surveys of Korean and Japanese markets for consideration under in-depth assessment topic *1-2 Genetic and other data for stock structure* and for the purposes of Pre-Implementation Assessment. The analyses will be based on up to 4 datasets, described below. These datasets, as Microsoft Excel spreadsheets, will be submitted on request to the Secretariat of the International Whaling Commission for distribution by the Data Availability Group. Note, File #2, submitted previously on 9 February 2005, is here superseded by Vs3. Two datasets are still in preparation. Descriptions of the files are included in the attached document.

File #1: Ja99_04_minkemtDNA_IWC05_Vs2.xls

File #2: Ko99_03_minkemtDNA_IWC05_Vs3.xls [revised]

File #3: Ko04_05_minkemtDNA_IWC09_Vs1.xls [in preparation]

File #4: Ko_pre99_minkemtDNA_IWC09_Vs1.xls [in preparation]

As the Pre-Implementation Assessment is intended to provide advice to the Committee on catch limits, we assume that the Data Availability Group will consider requests for access to the datasets under conditions of Procedure A of *Annex T* (JCRM Volume 6 2004, Report of the Working Group on Data Availability). Anyone viewing these data is subject to these conditions and to the accompanying Data Availability Protocol for the Cetacean Conservation and Genetic Laboratory of OSU (see attached), unless otherwise specifically agreed with me in writing.

Sincerely,



C. Scott Baker
Associate Director, Marine Mammal Institute
Professor, Fisheries and Wildlife

File #1: Ja99_04_minkemtDNA_IWC05_Vs2.xls

Abstract: Genetic information (sex, mtDNA haplotypes and haplogroups) from products purchased on Japanese markets during 9 surveys from February 1999 to February 2004, and identified as North Pacific minke whales (n = 147 market individuals as updated from SC/56/BC4).

Data provider: C.S. Baker, Laboratory of Molecular Ecology and Evolution, University of Auckland, New Zealand

Contact: C. S. Baker, email: cs.baker@auckland.ac.nz

Contributors: C.S. Baker, F. Cipriano, M.L. Dalebout, N. Funahashi, S. Lavery and G. Lento

References:

2009. Lukoschek V, Funahashi N, Lavery S, Dalebout ML, Cipriano F, Baker CS. 'High proportion of protected minke whales sold on Japanese markets is due to illegal, unreported or unregulated exploitation'. *Animal Conservation* 12:385-395

2004. Lavery, S., Funahashi, N., Ma, Y-U., Dalebout, M.L., MacInnes, H. and Baker, C.S. mtDNA diversity and individual identification of North Pacific minke whales from coastal waters of Japan and Korea. SC/56/BC4 report to the Scientific Committee of the International Whaling Commission.

2002. Dalebout, M. L., Lento, G. M., Cipriano, F., N. Funahashi, and Baker, C. S. 'How many protected minke whales are sold in Japan and Korea? A census by DNA profiling'. *Animal Conservation* 5: 143-152.

2000. Baker, C. S., Lento, G. L., Cipriano, F. & Palumbi, S. R. 'Predicted decline of protected whales based on molecular genetic monitoring of Japanese and Korean markets'. *Proceedings of the Royal Society, London B* 267:1191-1199.

Description: A single Microsoft Excel file includes three worksheets: 1) Read Me; 2) Reference sequence; and 3) Primary Data. Read Me contains this description. The Reference sequence contains the GenBank format of a sample representing the most common haplotype of the Korean or 'J' stock (Back99.02, GenBank# AY878077) used to designate the position of variable sites. The Primary Data includes the following information:

- 1) **Sample code** of market individual, as region (J for Japan), year and accession number. Where microsatellite genotyping confirmed replicate samples of market individuals, the first purchase has been chosen as the individual code.
- 2) **Sex** as identified by molecular markers.
- 3) **Haplotype/Variable sites** of samples, based on 32 variable sites in the first 463 base pairs of the mtDNA control region. Variable sites are shown in the conventional 'match to first' format, where a '.' indicates a match to the reference sequence and a '?' indicates missing data. The reference sequence is Back99.02 (GenBank# AY878077), the most common haplotype of the Korean or 'J' stock. All variable sites have been reviewed and confirmed except where indicated. No insertions or deletions have been detected in the sequences identified as originating from the North Pacific minke whales.
- 4) **Haplogroup** of the sample, based on nucleotide position 298 and 463 of the 32 variable sites of the mtDNA control region, as used previously to differentiate between the J and O stocks. The haplogroup is available for a small number of samples for which haplotype information is not available. The absence of this information is indicated by a '?' in all other positions.
- 5) **Purchase date**.
- 6) **Survey date** as shown in SC/56/BC4.
- 7) **Location of purchase (prefecture)**.

File #2: Ko99_03_minkemtDNA_IWC05_Vs3.xls [Note: This file supersedes the previous file submitted to the DAG on 9 February 2009]

Abstract: Genetic information (sex, mtDNA haplotypes, as defined by variable sites, and haplogroups) from products purchased on markets in the Republic of Korea during 12 surveys from March 1999 to December 2003, and identified as North Pacific minke whales (n = 205 market individuals as updated from Baker et al. 2007).

Data provider: C.S. Baker, Marine Mammal Institute, Oregon State University

Contact: C. S. Baker, email: scott.baker@oregonstate.edu

Contributors: C.S. Baker, R.L. Brownell, M.L. Dalebout, N. Funahashi, S. Lavery G. Lento, Ma Yong-Un and K. Robertson

References:

2007. Baker CS, Cooke JG, Lavery S, Dalebout ML, Ma Y-U, Funahashi N, Carraher C, Brownell RL. 'Estimating the number of whales entering trade using DNA profiling and capture-recapture analysis of market products'. *Molecular Ecology* 16:2617-2626
2004. Lavery, S., Funahashi, N., Ma, Y-U., Dalebout, M.L., MacInnes, H. and Baker, C.S. mtDNA diversity and individual identification of North Pacific minke whales from coastal waters of Japan and Korea. SC/56/BC4 report to the Scientific Committee of the International Whaling Commission.
2002. Dalebout, M. L., Lento, G. M., Cipriano, F., N. Funahashi, and Baker, C. S. 'How many protected minke whales are sold in Japan and Korea? A census by DNA profiling'. *Animal Conservation* 5: 143-152.
2000. Baker, C. S., Lento, G. L., Cipriano, F. & Palumbi, S. R. 'Predicted decline of protected whales based on molecular genetic monitoring of Japanese and Korean markets'. *Proceedings of the Royal Society, London B* 267:1191-1199.

Description: A single Microsoft Excel file includes three worksheets: 1) Read Me; 2) Reference sequence; and 3) Primary Data. Read Me contains this description. The Reference sequence contains the GenBank format of a sample representing the most common haplotype of the Korean or 'J' stock (Back99.02, GenBank# AY878077) used to designate the position of variable sites. The Primary Data includes the following information:

- 1) **Sample code** of market individual, as region (K for Korea), year and accession number. Where microsatellite genotyping confirmed replicate samples of market individuals, the first purchase has been chosen as the individual code.
- 2) **Sex** as identified by molecular markers.
- 3) **Haplotype/Variable sites** of samples, based on 32 variable sites in the first 463 base pairs of the mtDNA control region. Variable sites are shown in the conventional 'match to first' format, where a '.' indicates a match to the reference sequence and a '?' indicates missing data. The reference sequence is Back99.02 (GenBank# AY878077), the most common haplotype of the Korean or 'J' stock. All variable sites have been reviewed and confirmed except where indicated. No insertions or deletions have been detected in the sequences identified as originating from the North Pacific minke whales.
- 4) **Haplogroup** of the sample, based on nucleotide position 298 and 463 of the 32 variable sites of the mtDNA control region, as used previously to differentiate between the J and O stocks. The haplogroup is available for a small number of samples for which haplotype information is not available. The absence of this information is indicated by a '?' in all other positions.
- 5) **Purchase date**.
- 6) **Survey date** as shown in SC/56/BC4. All samples were purchased in the cities of Busan, Ulsan or Pohang.

File #3: Ko04_05_minkemtdNA_IWC09_Vs1.xls

Abstract: Genetic information (sex, mtDNA haplotypes, as defined by variable sites, and haplogroups) from products purchased on markets in the Republic of Korea during 7 surveys from February 2004 to February 2005, and identified as North Pacific minke whales (n ~ 80 market individuals, to be confirmed by ongoing review of genotypes).

Data provider: C.S. Baker, Marine Mammal Institute, Oregon State University

Contact: C. S. Baker, email: scott.baker@oregonstate.edu

Contributors: C.S. Baker, N. Funahashi, Ma Yong-Un

References:

Baker CS, Lukoschek V, Lavery S, Dalebout ML, Yong-un M, Endo T, Funahashi N (2006) Incomplete reporting of whale, dolphin and porpoise 'bycatch' revealed by molecular monitoring of Korean markets. *Animal Conservation* 9:474-482

Description: A single Microsoft Excel file includes three worksheets: 1) Read Me; 2) Reference sequence; and 3) Primary Data. Read Me contains this description. The Reference sequence contains the GenBank format of a sample representing the most common haplotype of the Korean or 'J' stock (Back99.02, GenBank# AY878077) used to designate the position of variable sites. The Primary Data includes the following information:

- 1) **Sample code** of market individual, as region (K for Korea), year and accession number. Where microsatellite genotyping confirmed replicate samples of market individuals, the first purchase has been chosen as the individual code.
- 2) **Sex** as identified by molecular markers.
- 3) **Haplotype/Variable sites** of samples, based on 32 variable sites in the first 463 base pairs of the mtDNA control region. Variable sites are shown in the conventional 'match to first' format, where a '.' indicates a match to the reference sequence and a '?' indicates missing data. The reference sequence is Back99.02 (GenBank# AY878077), the most common haplotype of the Korean or 'J' stock. All variable sites have been reviewed and confirmed except where indicated. No insertions or deletions have been detected in the sequences identified as originating from the North Pacific minke whales.
- 4) **Haplogroup** of the sample, based on nucleotide position 298 and 463 of the 32 variable sites of the mtDNA control region, as used previously to differentiate between the J and O stocks. The haplogroup is available for a small number of samples for which haplotype information is not available. The absence of this information is indicated by a '?' in all other positions.
- 5) **Purchase date.**
- 6) **Survey date** as shown in SC/56/BC4. All samples were purchased in the cities of Busan, Ulsan or Pohang.

File #4: Ko_pre99_minkemtDNA_IWC09_Vs1.xls

Abstract: Genetic information (sex, mtDNA haplotypes, as defined by variable sites, and haplogroups) from products purchased on markets in the Republic of Korea prior to 1999, and identified as North Pacific mink whales (number to be determined by ongoing review).

Data provider: C.S. Baker, Marine Mammal Institute, Oregon State University

Contact: C. S. Baker, email: scott.baker@oregonstate.edu

Contributors: C.S. Baker, N. Funahashi,

References:

2000. Baker, C. S., Lento, G. L., Cipriano, F. & Palumbi, S. R. 'Predicted decline of protected whales based on molecular genetic monitoring of Japanese and Korean markets'. *Proceedings of the Royal Society, London B* 267:1191-1199.

Description: A single Microsoft Excel file includes three worksheets: 1) Read Me; 2) Reference sequence; and 3) Primary Data. Read Me contains this description. The Reference sequence contains the GenBank format of a sample representing the most common haplotype of the Korean or 'J' stock (Back99.02, GenBank# AY878077) used to designate the position of variable sites. The Primary Data includes the following information:

- 1) **Sample code** of market individual, as region (K for Korea), year and accession number. Where microsatellite genotyping confirmed replicate samples of market individuals, the first purchase has been chosen as the individual code.
- 2) **Sex** as identified by molecular markers.
- 3) **Haplotype/Variable sites** of samples, based on 32 variable sites in the first 463 base pairs of the mtDNA control region. Variable sites are shown in the conventional 'match to first' format, where a '.' indicates a match to the reference sequence and a '?' indicates missing data. The reference sequence is Back99.02 (GenBank# AY878077), the most common haplotype of the Korean or 'J' stock. All variable sites have been reviewed and confirmed except where indicated. No insertions or deletions have been detected in the sequences identified as originating from the North Pacific minke whales.
- 4) **Haplogroup** of the sample, based on nucleotide position 298 and 463 of the 32 variable sites of the mtDNA control region, as used previously to differentiate between the J and O stocks. The haplogroup is available for a small number of samples for which haplotype information is not available. The absence of this information is indicated by a '?' in all other positions.
- 5) **Purchase date.**